

Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-856-070-19 (1-13) x AX411074 (1-3044)

QY 1 LysGluGluLeuMetLeuAroLeuGlnAspTyrGluGlu 13
|||||
DB 1147 AAGGAGGACTTCATCCCTCCGCTCCAGGACATATGAGGAG 1185

RESULT 4
HSEZRIN 3044 bp mRNA linear PRI 12-SEP-1993

LOCUS Human mRNA for ezrin.
DEFINITION X51521

ACCESSION X51521 1 GI:31282

VERSION ezrin; kinase substrate; microvilli protein.
KEYWORDS Homo sapiens.

SOURCE Homo sapiens.
ORGANISM Homo sapiens.

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Hunter, T.
TITLE Direct Submission

JOURNAL Submitted (25-JAN-1990) Hunter T., The Salk Institute, Molecular
Biology and Virology Laboratory, 10010 North Torrey Pines Road, San
Diego, CA 92138, USA

REFERENCE 2 (bases 1 to 3044)
AUTHORS Gould, K.L., Bretscher, A., Esch, F.S. and Hunter, T.

TITLE cDNA cloning and sequencing of the protein-tyrosine kinase
substrate, ezrin, reveals homology to band 4.1

JOURNAL EMBO J. 8 (13), 4133-4142 (1989)

MEDLINE EMO J. 8 (13) 4133-4142 (1989)
PUBMED 90076135

COMMENT 2591371
FEATURES See also

source location/Qualifiers
1..3044

/organism="Homo sapiens"
/db_xref="taxon:9606"

/clone="F6"
/cell_line="Hela"

/clone_lib="Okayama-Herg"
118 1878

/note="ezrin (AA 1-586)"
/codon_start=1

/protein_id="CAA35893.1"
/db_xref="GI:31283"

/translation="MPK1NVRVTMDAELETAIOPNTT-KOLFTOVKVTIGLPEVWY
FNIHYVKNKSPETWKLQKVSAGEVPEKNPIQKPAKFTYEDVAEELIDITQFLP
FLVKEGILSDIYCPETAVILGSAVQNKFGYKFKVSKYLSSERLTPQWVQ
HKLIDQWEDRIQWHAHRCMIKINAMIPYIKIADLPMYGNTHFKKKGIDHWL
GVDAIGNTYKDKKILPTKPTGFWSEIPIPTSPNKKFVPTIKKAPDVFYAPKPI
NKRILQICMGNHMLYMKRKKDDITFVQMKQAKREKHQKQLRQKQKREKRETE
REKQMKRREKFTIMRLQDYEEKTKAEKELSEQLQLEERKRAEAEAELEAD
RMAALRAKELEQAVDQIKSGQLAAEYIAKIALLEAARKEDEVEEMQHRAK
EADDLVKIKELHLVMTAPPVPPVPSVGVGSELSQRCAPTEPTYSALSSGI
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TLRIQKQNKIKIDPEAL"

1709..1711
/note="seq was fig in [1]"
/citation=[1]

old_sequence 826 a 687 c 855 g 675 t 1 others

BASE COUNT
ORIGIN

Alignment Scores:
Pred. No.: 0.000857 Length: 3044

Score: 65.00 Matches: 13

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-856-070-19 (1-13) x HSEZRIN (1-3044)

QY 1 LysGluGluLeuMetLeuAroLeuGlnAspTyrGluGlu 13
|||||
DB 1147 AAGGAGGACTTCATCCCTCCGCTCCAGGACATATGAGGAG 1185

RESULT 5
LOCUS AX440476 3047 bp DNA linear PAT 28 JUN 2002

DEFINITION Sequence 329 from Patent WO0190154.
ACCESSION AX440476

VERSION AX440476.1 GI:21665286

KEYWORDS human.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Xu, J., Mitcham, J.L., Harlocker, S.L., Dillon, D.C., Secretist, H.,
Lodes, M.J., Algate, P.A., Fling, S.P., Mannion, J.F., Benson, D.R. and
Carter, D.

TITLE Compositions and methods for the therapy and diagnosis of ovarian
cancer

JOURNAL PATENT: WO 0190154-A 329 29-NOV-2001;
COPICA COPPATION (US)

FEATURES Location/Qualifiers
1..3047

source /organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 828 a 687 c 856 g 675 t 1 others

ORIGIN

Alignment Scores:
Pred. No.: 0.000857 Length: 3047

Score: 65.00 Matches: 13

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-856-070-19 (1-13) x AX440476 (1-3047)

QY 1 LysGluGluLeuMetLeuAroLeuGlnAspTyrGluGlu 13
|||||
DB 1147 AAGGAGGACTTCATCCCTCCGCTCCAGGACATATGAGGAG 1185

RESULT 6
LOCUS HSM802625 4072 bp mpna linear FRI 23 MAR 2000

DEFINITION Hpsc sapiens mpna; cDNA DKFZ762H157 (from clone DKFZ762H157);
complete cds.

ACCESSION AL162086
VERSION AL162086.1 GI:7428174

KEYWORDS Homo sapiens.
SOURCE Homo sapiens.

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4072)
AUTHORS Ottenwälder, B., Obermaier, B., Mewes, H.W., Weil, H. and Wiemann, S.

TITLE Direct Submission
JOURNAL Submitted (15-MAR-2000) MIPS, Am Klemperspitze 16a, D-92152
Martinsried GERMANY

COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
sequenced by MedGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
(DKFZ762H157) is available at the RZPD in Berlin. Please contact
the RZPD, Postfach 101550, D-10585 Berlin, Germany.

Information about the clone and the sequencing project is available
at <http://www.mips.biochem.mpg.de/frag/cDNA/>.

FEATURES Location/Qualifiers
1..3072


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* 187911 190625: contig of 2715 bp in length
* 190626 190645: gap of unknown length
* 190646 192088: contig of 1443 bp in length
* 192089 192198: gap of unknown length
* 192199 193637: contig of 1529 bp in length
* 193638 193657: gap of unknown length
* 193658 195040: contig of 1383 bp in length
* 195041 195060: gap of unknown length
* 195061 196945: contig of 1885 bp in length
* 196946 196965: gap of unknown length
* 196966 198219: contig of 1254 bp in length
* 198220 198239: gap of unknown length
* 198240 199307: contig of 1668 bp in length
* 199308 199927: gap of unknown length
* 199928 201164: contig of 1236 bp in length
* 201165 201183: gap of unknown length
* 201184 202027: contig of 844 bp in length
* 202028 202047: gap of unknown length
* 202048 202902: contig of 855 bp in length
* 202903 202922: gap of unknown length
* 202923 204153: contig of 1228 bp in length
* 204154 204173: gap of unknown length
* 204174 205707: contig of 1537 bp in length
* 205708 205727: gap of unknown length
* 205728 207782: contig of 2055 bp in length.

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FEATURES

```

source
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/organism="Mus musculus"
/strain="C57BL6/J"
/db_xref="taxon:10090"
/chromosome="15"
/clone="pp24-103120"
/sex="male"
BASE COUNT 54791 a 49882 c 49733 g 53275 + 3101 others
ORIGIN

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Alignment Scores:
Pred. No.: 0.333 Length: 207782
Score: 62.00 Matches: 12
Percent Similarity: 100.00% Conservations: 1
Best Local Similarity: 92.31% Mismatches: 0
Query Match: 95.38% Indels: 0
Eh: 2 Gaps: 0

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US-09-856-070-19 (1-13) x AC074334 (1-207792)

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QY 1 TysGluGluLeuMetLeuArgLeuGlnAspTyrGlnGlu 13
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Db 173053 AAGGAGAGGTGATGCTTGCGTTCGAGACATAGAGACAG 173015

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RESULT 13

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AC022329/c 217917 bp DNA linear HTC 15-MAY-2002
LOCUS Mus musculus clone PP24-103120 strain C57BL6/J, WORKING DRAFT
DEFINITION
SEQUENCE, 11 unordered pieces.
AC022329
AC022329.8 GI:118057360
HTG: HTGS_PHASE1: HTGS_DRAFT.

```

```

SOURCE
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
1 (bases 1 to 217917)
Montgomery,K.P., Grills,G., Han,J., Lee,P., Long,J., Pomaraty,P.,
Ioshikhes,I.P., Shim,C., Decker,J., Thomas,F., Perera,A.,
Gordon,M., Goltz,J.S. and Kucherlapati,R.
High Throughput Mouse Sequencing
Unpublished
2 (bases 1 to 217917)
Montgomery,K.P., Grills,G., Han,J., Lee,P., Long,J., Pomaraty,P.,
Ioshikhes,I.P., Shim,C., Decker,J., Thomas,F., Perera,A.,
Gordon,M., Goltz,J.S. and Kucherlapati,R.
Direct Submission

```

REFERENCE

```

AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE

```

JOURNAL

COMMENT

Submitted (01-FEB-2003) Department of Molecular Genetics, Albert Einstein College of Medicine Genome Center, 1300 Morris Park Ave., Bronx, NY 10461, USA
 On Jan 4, 2002 this sequence version replaced gi:11094413.

 --Genome Center
 Center: Harvard Partners Genome Center
 Center Code: HPGC
 Web site: <http://www.hpgc.org/Sequence/mouse.html>
 Contact: hgpcmodel.mgh.harvard.edu

 -----Summary Statistics
 Center project name: AAC
 Sequencing vector: pDC18; L08752
 Chemistry: Dye-terminator Big Dye; 100%
 *Consensus quality: 212564 at least Q20
 *Consensus quality: 211720 at least Q30
 *Consensus quality: 210397 at least Q40
 Estimated insert size: agarose-pp - N/A
 **Estimated insert size: 217717 - sum-of-connigs
 Quality coverage: agarose-pp - N/A
 Quality coverage: 8.5 x in Q20 bases; sum-of-connigs estimation

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 11 contigs, the true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

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1 60900: contig of 60900 bp in length
* 60901 60920: gap of unknown length
* 60921 106520: contig of 45600 bp in length
* 106521 106540: gap of unknown length
* 106541 142332: contig of 35782 bp in length
* 142333 142342: gap of unknown length
* 142343 176177: contig of 33835 bp in length
* 176178 176197: gap of unknown length
* 176198 204272: contig of 28075 bp in length
* 204273 204292: gap of unknown length
* 204293 209252: contig of 4960 bp in length
* 209253 209272: gap of unknown length
* 209273 214332: contig of 5060 bp in length
* 214333 214352: gap of unknown length
* 214353 215731: contig of 1379 bp in length
* 215732 215751: gap of unknown length
* 215752 215800: contig of 49 bp in length
* 215801 215820: gap of unknown length
* 215821 216675: contig of 855 bp in length
* 216676 216695: gap of unknown length
* 216696 217917: contig of 1222 bp in length.

```

FEATURES

```

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/organism="Mus musculus"
/strain="C57BL6/J"
/db_xref="taxon:10090"
/clone="pp24-103120"
/sex="male"
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60921..106520
/note="assembly_name:Contig210"
clone_end:SP6
vector_side:left"
106541..142332
/note="assembly_name:Contig209"
142343..176177
/note="assembly_name:Contig208"
clone_end:I7
vector_side:left"
176198..204272
/note="assembly_name:Contig207"
204293..209252
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misc_feature

misc_feature

misc_feature

misc_feature

misc_feature

misc_feature


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VERSION      AF188897.1  GI:6063144
KEYWORDS
SOURCE
ORGANISM      Homo sapiens.
               Homo sapiens
               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 475)
AUTHORS      Chen, Z.C., Fadiel, A. and Naittolin, P.
TITLE        Ezrin gene mutation in ovarian cancer
JOURNAL
REFERENCE    2 (bases 1 to 475)
AUTHORS      Chen, Z.C., Fadiel, A. and Naittolin, P.
TITLE        Direct Submission
JOURNAL
FEATURES
SOURCE
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               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /chromosome="6"
               /map="6q22-q27"
               /cell_line="Hix3"
               /cell_type="epithelial cancer cells"
               /tissue_type="ovary"
               <1..3475
               /note="villin 2; kinase substrate"
               /codon_start=2
               /product="ezrin"
               /protein_id="AAF03155.1"
               /db_xref="GI:6063145"
               /translation="TSMYGINYFEVKNKKGTLWIGVDALSLNIYEKDDKLPKIGEP
               WSEIRATSPDKKFKVTKPKDKKAPDFVYAPGLRINKRTIQLCMGNIHLYMRRKPD
               IEVQMKAKARFAKOKQLERQQLEFAKKKKKVFKKKKMMPEKEELMLKIQDIE"
BASE COUNT   154 a   90 c   136 g   93 t
ORIGIN
Alignment Scores:
Pred. No.:      0.00136      Length:      475
Score:          60.00      Matches:      12
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     92.31%      Indels:      0
Db:              9          Gaps:      0
US-09-856-070-19 (1-13) x AF188897 (1-475)
QY      1  LysGluGluLeuMetLeuArgLeuGlnAspTyrGlu 12
        |||||||
Db      440 AAGGAGGAGTTCATGCTGCGGCTGCGAGCTATGAA 475

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Search completed: January 16, 2003, 19:03:44
Job time : 1208.56 secs